

WO 2004/009762

FC-11-PCT.ST25.txt
SEQUENCE LISTING

<110> Brandt, Kevin S.

<120> FLEA AND TICK OCTOPAMINE RECEPTOR NUCLEIC ACID MOLECULES,
PROTEINS AND USES THEREOF

<130> FC-11-PCT

<140> not yet assigned

<141> 2003-07-11

<150> 60/319,402

<151> 2003-07-17

<150> 60/426,601

<151> 2003-11-15

<160> 50

<170> PatentIn version 3.2

<210> 1

<211> 111

<212> DNA

<213> Ctenocephalides felis

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gggactcata gccgggcttt gggttcttag ttttgtgatc tgcttccac c 111

<210> 2

<211> 111

<212> DNA

<213> Ctenocephalides felis

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tcgtagacat gatgctcgga taagcaactg gcctgggtgac agcgacatat c 111

<210> 3

<211> 2061

<212> DNA

<213> Ctenocephalides felis

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<220>

<221> misc_feature

<222> (192)..(192)

<223> The "Xaa" at location 192 = Ala or Thr

<220>

<221> misc_feature

<222> (193)..(193)

<223> The "Xaa" at location 193 = Asn or Tyr

FC-11-PCT.ST25.txt

<400> 3

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at aga tat gtc gct gtc acc agg cca gtt gct tat ccg agc atc atg      47
  Arg Tyr Val Ala Val Thr Arg Pro Val Ala Tyr Pro Ser Ile Met
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tct acg aaa agg gct aag gga ctc ata gcc ggg ctt tgg gtt ctt agt      95
Ser Thr Lys Arg Ala Lys Gly Leu Ile Ala Gly Leu Trp Val Leu Ser
          20             25             30

ttt gtg ata tgc ttt cca cct tta gtc gga tgg aaa gat aaa aag gaa      143
Phe Val Ile Cys Phe Pro Pro Leu Val Gly Trp Lys Asp Lys Lys Glu
          35             40             45

tcc gag gat ctg ata gac ata tct tca tgt cct tgg acg tgc gag ttg      191
Ser Glu Asp Leu Ile Asp Ile Ser Ser Cys Pro Trp Thr Cys Glu Leu
          50             55             60

acg aac gat gca gga tat gtg gtg tat tct gct ctc gga tca ttc tac      239
Thr Asn Asp Ala Gly Tyr Val Val Tyr Ser Ala Leu Gly Ser Phe Tyr
    65             70             75

att cct atg ttt gtc atg tta ttt ttc tac tgg agg ata tat aga gca      287
Ile Pro Met Phe Val Met Leu Phe Phe Tyr Trp Arg Ile Tyr Arg Ala
    80             85             90             95

gct gtc agg aca acc aga gct atc aac caa gga ttc agg act aca aaa      335
Ala Val Arg Thr Thr Arg Ala Ile Asn Gln Gly Phe Arg Thr Thr Lys
          100             105             110

ggg tgc cgt ggt ata gga cga ttt gac gaa caa cgc cta act tta agg      383
Gly Ser Arg Gly Ile Gly Arg Phe Asp Glu Gln Arg Leu Thr Leu Arg
          115             120             125

att cat aga gga cgg ggt ggt tct gaa aat aga aga tgt cat cat cat      431
Ile His Arg Gly Arg Gly Gly Ser Glu Asn Arg Arg Cys His His His
          130             135             140

tct tcc att aaa agt aat gct tca ggg aga atg tct aca tct aca tct      479
Ser Ser Ile Lys Ser Asn Ala Ser Gly Arg Met Ser Thr Ser Thr Ser
          145             150             155

atg agg aat tgt tct cct caa cat agt tca cca cgt agt gca agt acc      527
Met Arg Asn Cys Ser Pro Gln His Ser Ser Pro Arg Ser Ala Ser Thr
          160             165             170             175

agc tta gga agt act cac gaa tca cct gaa aaa tca tct ata tca agg      575
Ser Leu Gly Ser Thr His Glu Ser Pro Glu Lys Ser Ser Ile Ser Arg
          180             185             190

rcc wac acc tgg gtt ttg cat cat gcg acc aat aat tcc aat tca gga      623
Xaa Xaa Thr Trp Val Leu His His Ala Thr Asn Asn Ser Asn Ser Gly
          195             200             205

gct tgt aac caa gtc gtc att gcc aat aat aca agt caa agt gca cca      671
Ala Cys Asn Gln Val Val Ile Ala Asn Asn Thr Ser Gln Ser Ala Pro
          210             215             220

aac aat aat cag tta aat agt acc cag cct gar gtc act gtg aca aaa      719
Asn Asn Asn Gln Leu Asn Ser Thr Gln Pro Glu Val Thr Val Thr Lys
          225             230             235

agt agt cga aga tct tcg aaa tca tat aag agc ttt aaa aag gaa aga      767
Ser Ser Arg Arg Ser Ser Lys Ser Tyr Lys Ser Phe Lys Lys Glu Arg
          240             245             250             255

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gtt caa att tcg gtg cag tat cca agt gca gaa aga ctt gat gaa ttg	815
Val Gln Ile Ser Val Gln Tyr Pro Ser Ala Glu Arg Leu Asp Glu Leu	
260 265 270	
gaa ggt gaa tta gaa ggt gat gct aca aac aac atg tac acc gtc cac	863
Glu Gly Glu Leu Glu Gly Asp Ala Thr Asn Asn Met Tyr Thr Val His	
275 280 285	
tac tct gtg tcc aat ggt aac agc ttg tca aat cat tcg ttg atg cca	911
Tyr Ser Val Ser Asn Gly Asn Ser Leu Ser Asn His Ser Leu Met Pro	
290 295 300	
gag cag caa ata gtc gat tct tcg agc caa caa cag acc att aga gca	959
Glu Gln Gln Ile Val Asp Ser Ser Ser Gln Gln Thr Ile Arg Ala	
305 310 315	
aca aca aca att aac ggt gat cag caa tta aat tcg ggt tcc atc tat	1007
Thr Thr Thr Ile Asn Gly Asp Gln Gln Leu Asn Ser Gly Ser Ile Tyr	
320 325 330 335	
cgg cca cag gat aat cat cat ctc cga gtt acg tcg caa aga ttg gca	1055
Arg Pro Gln Asp Asn His His Leu Arg Val Thr Ser Gln Arg Leu Ala	
340 345 350	
ccg tcg cct aca ctg tcg aag gga atg cat agg cga tcc agc agc tgc	1103
Pro Ser Pro Thr Leu Ser Lys Gly Met His Arg Arg Ser Ser Cys	
355 360 365	
gat agt aga gat ttg gct ggg ttt caa tta tgc gaa agt tca agt cca	1151
Asp Ser Arg Asp Leu Ala Gly Phe Gln Leu Cys Glu Ser Ser Ser Pro	
370 375 380	
agt cca aca aga agg ata atg tct gga agt ctt tat cgt gat gat agc	1199
Ser Pro Thr Arg Arg Ile Met Ser Gly Ser Leu Tyr Arg Asp Asp Ser	
385 390 395	
gag tta ggt tcg act tcc aaa ctg cag cag caa aat aga aaa atg ggc	1247
Glu Leu Gly Ser Thr Ser Lys Leu Gln Gln Gln Asn Arg Lys Met Gly	
400 405 410 415	
aaa cgt aat ata aaa gct cag gtg aaa cgg ttt cga atg gag acg aaa	1295
Lys Arg Asn Ile Lys Ala Gln Val Lys Arg Phe Arg Met Glu Thr Lys	
420 425 430	
gct gcc aaa aca ctt gca ata att gtc ggt ggt ttt att gta tgc tgg	1343
Ala Ala Lys Thr Leu Ala Ile Ile Val Gly Gly Phe Ile Val Cys Trp	
435 440 445	
ttt ccc ttt ttc aca atg tac gta ata aga gca ttt tgt cca gac tgc	1391
Phe Pro Phe Phe Thr Met Tyr Val Ile Arg Ala Phe Cys Pro Asp Cys	
450 455 460	
att cat cct gtt ctc ttc tcg gtt cta ttc tgg ctc ggc tac tgc aat	1439
Ile His Pro Val Leu Phe Ser Val Leu Phe Trp Leu Gly Tyr Cys Asn	
465 470 475	
tct gcc atc aat ccg ctg att tat gca ctt ttt agc aaa gat ttc aga	1487
Ser Ala Ile Asn Pro Leu Ile Tyr Ala Leu Phe Ser Lys Asp Phe Arg	
480 485 490 495	
tac gcc ttc aag cgc atc att tgc aga tac tgc ttt tgt tgc ggt aat	1535
Tyr Ala Phe Lys Arg Ile Ile Cys Arg Tyr Cys Phe Cys Cys Gly Asn	
500 505 510	

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cgt acc gag gcc cag cac agc ggt gga gct ggt ggt tct aga aga ggg      1583
Arg Thr Glu Ala Gln His Ser Gly Gly Ala Gly Gly Ser Arg Arg Gly
          515                      520                      525

tcc gat gga tct caa atg aaa act aat ttt agg ttt aat acc agt ttt      1631
Ser Asp Gly Ser Gln, Met Lys Thr Asn Phe Arg Phe Asn Thr Ser Phe
          530                      535                      540

aat acc aaa aac tgc gtt cgt caa gat agt gat aat gat gtc aca aga      1679
Asn Thr Lys Asn Cys Val Arg Gln Asp Ser Asp Asn Asp Val Thr Arg
          545                      550                      555

tgacccgcag ctaatgtggg attgcagagt cgagtttgaa aaaagtctag tctcaaaatc      1739

tgtgcaatct tgtgaattaa aaggagtga taaagacaat cgtagagtgc cgtaaaaata      1799

ttttcatata atgaaaataa atcgtgaata tatcaaaaat aaattgtata agattgcatg      1859

taaatttaca gaaaattctt ccaaagtttt atcaatgttg gattatataa aatatgtcat      1919

gtaagtttta ttgagcaagc atttcaattt attgcctaaa tacaagtttt gttttcaata      1979

taaaatataa aatataaaaa ctgatgtaaa tagatgaaaa aataaattgt tatatttgaa      2039

taactaaaaa aaaaaaaaaa aa                                             2061

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<210> 4
<211> 559
<212> PRT
<213> Ctenocephalides felis

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<220>
<221> misc_feature
<222> (192)..(192)
<223> The 'Xaa' at location 192 stands for Ala, or Thr.

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<220>
<221> misc_feature
<222> (193)..(193)
<223> The 'Xaa' at location 193 stands for Asn, or Tyr.

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<400> 4

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Arg Tyr Val Ala Val Thr Arg Pro Val Ala Tyr Pro Ser Ile Met Ser
1          5          10          15

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Thr Lys Arg Ala Lys Gly Leu Ile Ala Gly Leu Trp Val Leu Ser Phe
          20          25          30

```

```

Val Ile Cys Phe Pro Pro Leu Val Gly Trp Lys Asp Lys Lys Glu Ser
          35          40          45

```

```

Glu Asp Leu Ile Asp Ile Ser Ser Cys Pro Trp Thr Cys Glu Leu Thr
          50          55          60

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Asn Asp Ala Gly Tyr Val Val Tyr Ser Ala Leu Gly Ser Phe Tyr Ile
          65          70          75          80

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Pro Met Phe Val Met Leu Phe Phe Tyr Trp Arg Ile Tyr Arg Ala Ala
 85 90 95

Val Arg Thr Thr Arg Ala Ile Asn Gln Gly Phe Arg Thr Thr Lys Gly
 100 105 110

Ser Arg Gly Ile Gly Arg Phe Asp Glu Gln Arg Leu Thr Leu Arg Ile
 115 120 125

His Arg Gly Arg Gly Gly Ser Glu Asn Arg Arg Cys His His His Ser
 130 135 140

Ser Ile Lys Ser Asn Ala Ser Gly Arg Met Ser Thr Ser Thr Ser Met
 145 150 155 160

Arg Asn Cys Ser Pro Gln His Ser Ser Pro Arg Ser Ala Ser Thr Ser
 165 170 175

Leu Gly Ser Thr His Glu Ser Pro Glu Lys Ser Ser Ile Ser Arg Xaa
 180 185 190

Xaa Thr Trp Val Leu His His Ala Thr Asn Asn Ser Asn Ser Gly Ala
 195 200 205

Cys Asn Gln Val Val Ile Ala Asn Asn Thr Ser Gln Ser Ala Pro Asn
 210 215 220

Asn Asn Gln Leu Asn Ser Thr Gln Pro Glu Val Thr Val Thr Lys Ser
 225 230 235 240

Ser Arg Arg Ser Ser Lys Ser Tyr Lys Ser Phe Lys Lys Glu Arg Val
 245 250 255

Gln Ile Ser Val Gln Tyr Pro Ser Ala Glu Arg Leu Asp Glu Leu Glu
 260 265 270

Gly Glu Leu Glu Gly Asp Ala Thr Asn Asn Met Tyr Thr Val His Tyr
 275 280 285

Ser Val Ser Asn Gly Asn Ser Leu Ser Asn His Ser Leu Met Pro Glu
 290 295 300

Gln Gln Ile Val Asp Ser Ser Ser Gln Gln Gln Thr Ile Arg Ala Thr
 305 310 315 320

Thr Thr Ile Asn Gly Asp Gln Gln Leu Asn Ser Gly Ser Ile Tyr Arg
 325 330 335

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Pro Gln Asp Asn His His Leu Arg Val Thr Ser Gln Arg Leu Ala Pro
 340 345 350

Ser Pro Thr Leu Ser Lys Gly Met His Arg Arg Ser Ser Ser Cys Asp
 355 360 365

Ser Arg Asp Leu Ala Gly Phe Gln Leu Cys Glu Ser Ser Ser Pro Ser
 370 375 380

Pro Thr Arg Arg Ile Met Ser Gly Ser Leu Tyr Arg Asp Asp Ser Glu
 385 390 395 400

Leu Gly Ser Thr Ser Lys Leu Gln Gln Gln Asn Arg Lys Met Gly Lys
 405 410 415

Arg Asn Ile Lys Ala Gln Val Lys Arg Phe Arg Met Glu Thr Lys Ala
 420 425 430

Ala Lys Thr Leu Ala Ile Ile Val Gly Gly Phe Ile Val Cys Trp Phe
 435 440 445

Pro Phe Phe Thr Met Tyr Val Ile Arg Ala Phe Cys Pro Asp Cys Ile
 450 455 460

His Pro Val Leu Phe Ser Val Leu Phe Trp Leu Gly Tyr Cys Asn Ser
 465 470 475 480

Ala Ile Asn Pro Leu Ile Tyr Ala Leu Phe Ser Lys Asp Phe Arg Tyr
 485 490 495

Ala Phe Lys Arg Ile Ile Cys Arg Tyr Cys Phe Cys Cys Gly Asn Arg
 500 505 510

Thr Glu Ala Gln His Ser Gly Gly Ala Gly Gly Ser Arg Arg Gly Ser
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Thr Lys Asn Cys Val Arg Gln Asp Ser Asp Asn Asp Val Thr Arg
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<210> 5
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 <212> DNA
 <213> Ctenocephalides felis

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FC-11-PCT.ST25.txt

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ggaagaattt tctgtaaatt tacatgcaat cttatacaat ttatttttga tatattcacg 240
atttattttc atttatatgaa aatatttttta cggcactcta cgattgtctt tattcactcc 300
ttttaattca caagattgca cagattttga gactagactt ttttcaaact cgactctgca 360
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ataacatgac aaacatagga atgtagaatg atccgagagc agaatacacc acatattcctg 1860
catcggttct caactcgcac gtccaaggac atgaagatat gtctatcaga tcctcggatt 1920
cctttttatc tttccatccg actaaagggt gaaagcatat cacaaaacta agaaccctaaa 1980

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gcccggctat gagtccctta gcccttttcg tagacatgat gctcggataa gcaactggcc 2040
tggtgacagc gacatatcta t 2061

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<210> 6
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<212> DNA
<213> Ctenocephalides felis
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<221> CDS
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FC-11-PCT.ST25.txt

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 Leu Asp Arg Tyr Val Ala Val Thr Arg Pro Val Ala Tyr Pro Ser Ile
 155 160 165

atg tct acg aaa ggg gct aag gga ttc ata gcc gg 868
 Met Ser Thr Lys Gly Ala Lys Gly Phe Ile Ala
 170 175

<210> 7
 <211> 178
 <212> PRT
 <213> Ctenocephalides felis

<400> 7

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 20 25 30

Thr Thr Leu Tyr Asn His Asp Gly Thr Glu Cys Pro Gln Ile Glu Asn
 35 40 45

Val Asp Trp Leu Ser Pro Ser Ser Leu Ala Ser Leu Thr Val Leu Leu
 50 55 60

Thr Ile Asp Leu Leu Val Ile Leu Gly Asn Cys Leu Val Ile Ala Ala
 65 70 75 80

Val Phe Cys Ser Ser Lys Leu Arg Ser Val Thr Asn Leu Phe Ile Val
 85 90 95

Ser Leu Ala Val Ala Asp Leu Met Val Gly Ile Ala Val Leu Pro Phe
 100 105 110

Ser Ala Thr Trp Glu Val Phe Lys Val Trp Ile Phe Gly Ser Ser Trp
 115 120 125

Cys Arg Ala Trp Leu Ala Leu Asp Val Trp Met Cys Thr Ala Ser Ile
 130 135 140

Leu Asn Leu Cys Ala Ile Ser Leu Asp Arg Tyr Val Ala Val Thr Arg
 145 150 155 160

Pro Val Ala Tyr Pro Ser Ile Met Ser Thr Lys Gly Ala Lys Gly Phe
 165 170 175

Ile Ala

FC-11-PCT.ST25.txt

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 atccacacgt ccagggctaa ccaggctctg caccagctgc ttccgaatat ccaaaccttg 180
 aagacttccc aagttgcgct aaaaggcaaa accgcgatgc cgaccatcaa atcggcgact 240
 gcaagtgaca ctatgaacaa gttggtcaca ctgcgcagtt tgctggagca gaacacggct 300
 gctatcacca gacaatttcc caggatcacc agcaaataca tggtcagcaa aaccgtgaga 360
 cttgccaaagg aagaaggact cagccaatcc acattttcaa tttgaggaca ttcagtccca 420
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 acttgttctt gagttataaa atccacatta tttgtatagg ttgagcacac taacatgaac 780
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<210> 9
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 <212> DNA
 <213> Ctenocephalides felis

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 gtgatcctgg gaaattgtct ggtgatagca gccgtgttct gtcacagcaa actgcgcagt 240
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FC-11-PCT.ST25.txt

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tcattctaca ttcttatgtt tgtcatgtta tttttctact ggaggatata tagagcagct      720
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ggacgatttg acgaacaacg cctaacttta aggattcata gaggacgggg tggttctgaa      840
aatagaagat gtcatcatca ttcttccatt aaaagcaatg cttcaggagg aatgtctaca      900
tctacttcta tgaggaattg ttctccacaa catagttcac cacgtagtgc aagtaccagc      960
ttaggaagta ctcacgaatc acctgaaaaa tcatctatat caaggaccaa cacctggggt      1020
ttgcatcatg cgaccaataa ttccaattct ggagcttgta accaagtagt tatcgccaat      1080
aatacaagtc aaagtgcacc aaacaatcag ttaaatagta gtgccagcc tgaagtcact      1140
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attaagcaac aacaacaatt aacggtgaat cagcaattaa attcgggttc catctatcgg      1440
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ttatgcgaaa gttcaagtcc aagtccaaca agaaggataa tgtctggaag tctttatcgt      1620
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agagcatttt gtccagactg cattcatcct gttctcttct cggttctatt ctggctcggc      1860
tactgcaatt ctgccatcaa tccgctgatt tatgcacttt ttagcaaaga ttttagatac      1920
gccttcaagc gcatcatttg cagatactgc ttttgttgcg gtaatcgtag cgaggcccag      1980
cacagcgggtg gagctggtgg ttctagaaga gggtcgatg gatctcaaata gaaaactaat      2040
tttaggttta ataccagttt taataccaaa aactgcgttc gt                                2082

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<210> 10

<211> 2082

<212> DNA

<213> Ctenocephalides felis

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accgcaacaa aagcagtatc tgcaaatgat gcgcttgaag gcgtatctaa aatctttgct      180

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FC-11-PCT.ST25.txt

aaaaagtgca taaatcagcg gattgatggc agaattgcag tagccgagcc agaatagaac	240
cgagaagaga acaggatgaa tgcagtctgg acaaaatgct cttattacgt acattgtgaa	300
aaagggaaac cagcatacaa taaaaccacc gacaattatt gcaagtgttt tggcagcttt	360
cgtctccatt cgaaaccgtt tcacctgagc ttttatatta cgtttgccca tttttctatt	420
ttgctgctgc agtttggaag tcgaacctaa ctgcgtatca tcacgataaa gacttcaga	480
cattatcctt cttgttggac ttggacttga actttcgcat aattgaaacc cagccaaatc	540
tctactatcg cagctgctgg atcgccatg cattcccttc gacagtgtag gcgacggtgc	600
caatctttgc gacgtaactc ggagatgatg attatcctgt ggccgataga tggaaccga	660
atttaattgc tgattcacgc ttaattgttg ttgttgctta atggctctgt gttggtcga	720
agaatcgact atttgctgct ctggcatcaa cgaatgattt gacaagctgt taccattgga	780
cacagagtag tggacggtgt acatgttgtt tgtagcatca ctttctaatt caccttcaa	840
ttcatcaagt ctttctgcac ttggatactg caccgaaatt tgaactcttt ctttcttaa	900
gctcttatat gatttcgaag atcttcgact actttttgtt acagtgactt caggctgggc	960
actactatth aactgattgt ttggtgcact ttgacttgta ttattggcga taactacttg	1020
gttacaagct ccagaattgg aattattggt cgcgatgatc aaaaccaggg tgttggtcct	1080
tgatatagat gatttttcag gtgattcgtg agtacttcct aagctggtac ttgcactacg	1140
tggtgaacta tgttgtggag aacaattcct catagaagta gatgtagaca ttctccctga	1200
agcattgctt ttaatggaag aatgatgatg acatcttcta ttttcagaac caccocgtcc	1260
tctatgaatc cttaaagtta ggcggtgttc gtcaaategt cctataccac gcgaaccttt	1320
tgtggtcctg aatcattggt tgatagctct ggtgtcctg acagctgctc tatatatect	1380
ccagtagaaa aataacatga caaacatagg aatgtagaat gatcctagag cagaatacac	1440
cacatatect gcatcattcg tcaactcgca cgtccacgga catgaagata tgtctatcag	1500
atcctcggat tcctttttat ccttccatcc gactaaaggt ggaaaacata tcacaaaact	1560
aagaacccaa agcccggtta tgagtcctt agcccttttc gtagacatga tgctcggata	1620
agcaactggc ctggtgacag cgacatatct atccaaggat attgcgcaca gatttaatat	1680
cgaagctgtg cacatccaca cgtccagggc taaccaggct cggcaccagc tgcttccgaa	1740
tatccaaacc ttgaagactt cccaagttgc gctaaaaggc aaaaccgcga tgccgaccat	1800
caaateggcg actgcaagtg aactatgaa caagttggtc aactgcgca gtttgctgga	1860
gcagaacacg gctgctatca ccagacaatt tcccaggatc accagcaaatt cgatggtcag	1920
caaaaccgtg agacttgcta aggaagaagg actcagccag tcgacatttt caatttgagg	1980
acattcagtc ccatcatggt tgtacaaagt tgtcgaattt ccctgtcctg tggtaatggt	2040
tgccccagat aaggaagtcc cataacttag cctgattgtt gt	2082

FC-11-PCT.ST25.txt

<210> 11
 <211> 2136
 <212> DNA
 <213> Ctenocephalides felis

<220>
 <221> CDS
 <222> (1)..(2136)

<400> 11
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 1 5 10 15
 ggg act tcc tta tct ggg gca acc att acc aca gga cag gga aat tcg 96
 Gly Thr Ser Leu Ser Gly Ala Thr Ile Thr Thr Gly Gln Gly Asn Ser
 20 25 30
 aca act ttg tac aac cat gat ggg act gaa tgt cct caa att gaa aat 144
 Thr Thr Leu Tyr Asn His Asp Gly Thr Glu Cys Pro Gln Ile Glu Asn
 35 40 45
 gtc gac tgg ctg agt cct tct tcc tta gca agt ctc acg gtt ttg ctg 192
 Val Asp Trp Leu Ser Pro Ser Ser Leu Ala Ser Leu Thr Val Leu Leu
 50 55 60
 acc atc gat ttg ctg gtg atc ctg gga aat tgt ctg gtg ata gca gcc 240
 Thr Ile Asp Leu Leu Val Ile Leu Gly Asn Cys Leu Val Ile Ala Ala
 65 70 75 80
 gtg ttc tgc tcc agc aaa ctg cgc agt gtg acc aac ttg ttc ata gtg 288
 Val Phe Cys Ser Ser Lys Leu Arg Ser Val Thr Asn Leu Phe Ile Val
 85 90 95
 tca ctt gca gtc gcc gat ttg atg gtc ggc atc gcg gtt ttg cct ttt 336
 Ser Leu Ala Val Ala Asp Leu Met Val Gly Ile Ala Val Leu Pro Phe
 100 105 110
 agc gca act tgg gaa gtc ttc aag gtt tgg ata ttc gga agc agc tgg 384
 Ser Ala Thr Trp Glu Val Phe Lys Val Trp Ile Phe Gly Ser Ser Trp
 115 120 125
 tgc cga gcc tgg tta gcc ctg gac gtg tgg atg tgc aca gct tcg ata 432
 Cys Arg Ala Trp Leu Ala Leu Asp Val Trp Met Cys Thr Ala Ser Ile
 130 135 140
 tta aat ctg tgc gca ata tcc ttg gat aga tat gtc gct gtc acc agg 480
 Leu Asn Leu Cys Ala Ile Ser Leu Asp Arg Tyr Val Ala Val Thr Arg
 145 150 155 160
 cca gtt gct tat ccg agc atc atg tct acg aaa agg gct aag gga ctc 528
 Pro Val Ala Tyr Pro Ser Ile Met Ser Thr Lys Arg Ala Lys Gly Leu
 165 170 175
 ata gcc ggg ctt tgg gtt ctt agt ttt gtg ata tgt ttt cca cct tta 576
 Ile Ala Gly Leu Trp Val Leu Ser Phe Val Ile Cys Phe Pro Pro Leu
 180 185 190
 gtc gga tgg aag gat aaa aag gaa tcc gag gat ctg ata gac ata tct 624
 Val Gly Trp Lys Asp Lys Lys Glu Ser Glu Asp Leu Ile Asp Ile Ser
 195 200 205

FC-11-PCT.ST25.txt

tca tgt ccg tgg acg tgc gag ttg acg aat gat gca gga tat gtg gtg Ser Cys Pro Trp Thr Cys Glu Leu Thr Asn Asp Ala Gly Tyr Val Val 210 215 220	672
tat tct gct cta gga tca ttc tac att cct atg ttt gtc atg tta ttt Tyr Ser Ala Leu Gly Ser Phe Tyr Ile Pro Met Phe Val Met Leu Phe 225 230 235 240	720
ttc tac tgg agg ata tat aga gca gct gtc agg aca acc aga gct atc Phe Tyr Trp Arg Ile Tyr Arg Ala Ala Val Arg Thr Thr Arg Ala Ile 245 250 255	768
aac caa gga ttc agg acc aca aaa ggt tcg cgt ggt ata gga cga ttt Asn Gln Gly Phe Arg Thr Thr Lys Gly Ser Arg Gly Ile Gly Arg Phe 260 265 270	816
gac gaa caa cgc cta act tta agg att cat aga gga cgg ggt ggt tct Asp Glu Gln Arg Leu Thr Leu Arg Ile His Arg Gly Arg Gly Gly Ser 275 280 285	864
gaa aat aga aga tgt cat cat cat tct tcc att aaa agc aat gct tca Glu Asn Arg Arg Cys His His His Ser Ser Ile Lys Ser Asn Ala Ser 290 295 300	912
ggg aga atg tct aca tct act tct atg agg aat tgt tct cca caa cat Gly Arg Met Ser Thr Ser Thr Ser Met Arg Asn Cys Ser Pro Gln His 305 310 315 320	960
agt tca cca cgt agt gca agt acc agc tta gga agt act cac gaa tca Ser Ser Pro Arg Ser Ala Ser Thr Ser Leu Gly Ser Thr His Glu Ser 325 330 335	1008
cct gaa aaa tca tct ata tca agg acc aac acc tgg gtt ttg cat cat Pro Glu Lys Ser Ser Ile Ser Arg Thr Asn Thr Trp Val Leu His His 340 345 350	1056
gcg acc aat aat tcc aat tct gga gct tgt aac caa gta gtt atc gcc Ala Thr Asn Asn Ser Asn Ser Gly Ala Cys Asn Gln Val Val Ile Ala 355 360 365	1104
aat aat aca agt caa agt gca cca aac aat cag tta aat agt agt gcc Asn Asn Thr Ser Gln Ser Ala Pro Asn Asn Gln Leu Asn Ser Ser Ala 370 375 380	1152
cag cct gaa gtc act gta aca aaa agt agt cga aga tct tcg aaa tca Gln Pro Glu Val Thr Val Thr Lys Ser Ser Arg Arg Ser Ser Lys Ser 385 390 395 400	1200
tat aag agc ttt aag aag gaa aga gtt caa att tcg gtg cag tat cca Tyr Lys Ser Phe Lys Lys Glu Arg Val Gln Ile Ser Val Gln Tyr Pro 405 410 415	1248
agt gca gaa aga ctt gat gaa ttg gaa ggt gaa tta gaa ggt gat gct Ser Ala Glu Arg Leu Asp Glu Leu Glu Gly Glu Leu Glu Gly Asp Ala 420 425 430	1296
aca aac aac atg tac acc gtc cac tac tct gtg tcc aat ggt aac agc Thr Asn Asn Met Tyr Thr Val His Tyr Ser Val Ser Asn Gly Asn Ser 435 440 445	1344
ttg tca aat cat tcg ttg atg cca gag cag caa ata gtc gat tct tcg Leu Ser Asn His Ser Leu Met Pro Glu Gln Gln Ile Val Asp Ser Ser 450 455 460	1392

FC-11-PCT.ST25.txt

agc caa caa cag acc att aag caa caa caa caa tta acg gtg aat cag Ser Gln Gln Gln Thr Ile Lys Gln Gln Gln Gln Leu Thr Val Asn Gln 465 470 475 480	1440
caa tta aat tcg ggt tcc atc tat cgg cca cag gat aat cat cat ctc Gln Leu Asn Ser Gly Ser Ile Tyr Arg Pro Gln Asp Asn His His Leu 485 490 495	1488
cga gtt acg tcg caa aga ttg gca cgg tcg cct aca ctg tcg aag gga Arg Val Thr Ser Gln Arg Leu Ala Pro Ser Pro Thr Leu Ser Lys Gly 500 505 510	1536
atg cat agg cga tcc agc agc tgc gat agt aga gat ttg gct ggg ttt Met His Arg Arg Ser Ser Ser Cys Asp Ser Arg Asp Leu Ala Gly Phe 515 520 525	1584
caa tta tgc gaa agt tca agt cca agt cca aca aga agg ata atg tct Gln Leu Cys Glu Ser Ser Ser Pro Ser Pro Thr Arg Arg Ile Met Ser 530 535 540	1632
gga agt ctt tat cgt gat gat agc gag tta ggt tcg act tcc aaa ctg Gly Ser Leu Tyr Arg Asp Asp Ser Glu Leu Gly Ser Thr Ser Lys Leu 545 550 555 560	1680
cag cag caa aat aga aaa atg ggc aaa cgt aat ata aaa gct cag gtg Gln Gln Gln Asn Arg Lys Met Gly Lys Arg Asn Ile Lys Ala Gln Val 565 570 575	1728
aaa cgg ttt cga atg gag acg aaa gct gcc aaa aca ctt gca ata att Lys Arg Phe Arg Met Glu Thr Lys Ala Ala Lys Thr Leu Ala Ile Ile 580 585 590	1776
gtc ggt ggt ttt att gta tgc tgg ttt ccc ttt ttc aca atg tac gta Val Gly Gly Phe Ile Val Cys Trp Phe Pro Phe Phe Thr Met Tyr Val 595 600 605	1824
ata aga gca ttt tgt cca gac tgc att cat cct gtt ctc ttc tcg gtt Ile Arg Ala Phe Cys Pro Asp Cys Ile His Pro Val Leu Phe Ser Val 610 615 620	1872
cta ttc tgg ctc ggc tac tgc aat tct gcc atc aat ccg ctg att tat Leu Phe Trp Leu Gly Tyr Cys Asn Ser Ala Ile Asn Pro Leu Ile Tyr 625 630 635 640	1920
gca ctt ttt agc aaa gat ttt aga tac gcc ttc aag cgc atc att tgc Ala Leu Phe Ser Lys Asp Phe Arg Tyr Ala Phe Lys Arg Ile Ile Cys 645 650 655	1968
aga tac tgc ttt tgt tgc ggt aat cgt acc gag gcc cag cac agc ggt Arg Tyr Cys Phe Cys Cys Gly Asn Arg Thr Glu Ala Gln His Ser Gly 660 665 670	2016
gga gct ggt ggt tct aga aga ggg tcc gat gga tct caa atg aaa act Gly Ala Gly Gly Ser Arg Arg Gly Ser Asp Gly Ser Gln Met Lys Thr 675 680 685	2064
aat ttt agg ttt aat acc agt ttt aat acc aaa aac tgc gtt cgt caa Asn Phe Arg Phe Asn Thr Ser Phe Asn Thr Lys Asn Cys Val Arg Gln 690 695 700	2112
gat agt gat aat gat gtc aca aga Asp Ser Asp Asn Asp Val Thr Arg 705 710	2136

FC-11-PCT.ST25.txt

<210> 12
 <211> 712
 <212> PRT
 <213> Ctenocephalides felis

<400> 12

Met Asn Ala Ser Glu Tyr Ile Asn Thr Thr Thr Ile Arg Leu Ser Tyr
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Gly Thr Ser Leu Ser Gly Ala Thr Ile Thr Thr Gly Gln Gly Asn Ser
 20 25 30

Thr Thr Leu Tyr Asn His Asp Gly Thr Glu Cys Pro Gln Ile Glu Asn
 35 40 45

Val Asp Trp Leu Ser Pro Ser Ser Leu Ala Ser Leu Thr Val Leu Leu
 50 55 60

Thr Ile Asp Leu Leu Val Ile Leu Gly Asn Cys Leu Val Ile Ala Ala
 65 70 75 80

Val Phe Cys Ser Ser Lys Leu Arg Ser Val Thr Asn Leu Phe Ile Val
 85 90 95

Ser Leu Ala Val Ala Asp Leu Met Val Gly Ile Ala Val Leu Pro Phe
 100 105 110

Ser Ala Thr Trp Glu Val Phe Lys Val Trp Ile Phe Gly Ser Ser Trp
 115 120 125

Cys Arg Ala Trp Leu Ala Leu Asp Val Trp Met Cys Thr Ala Ser Ile
 130 135 140

Leu Asn Leu Cys Ala Ile Ser Leu Asp Arg Tyr Val Ala Val Thr Arg
 145 150 155 160

Pro Val Ala Tyr Pro Ser Ile Met Ser Thr Lys Arg Ala Lys Gly Leu
 165 170 175

Ile Ala Gly Leu Trp Val Leu Ser Phe Val Ile Cys Phe Pro Pro Leu
 180 185 190

Val Gly Trp Lys Asp Lys Lys Glu Ser Glu Asp Leu Ile Asp Ile Ser
 195 200 205

Ser Cys Pro Trp Thr Cys Glu Leu Thr Asn Asp Ala Gly Tyr Val Val
 210 215 220

FC-11-PCT.ST25.txt

Tyr Ser Ala Leu Gly Ser Phe Tyr Ile Pro Met Phe Val Met Leu Phe
 225 230 235 240
 Phe Tyr Trp Arg Ile Tyr Arg Ala Ala Val Arg Thr Thr Arg Ala Ile
 245 250 255
 Asn Gln Gly Phe Arg Thr Thr Lys Gly Ser Arg Gly Ile Gly Arg Phe
 260 265 270
 Asp Glu Gln Arg Leu Thr Leu Arg Ile His Arg Gly Arg Gly Gly Ser
 275 280 285
 Glu Asn Arg Arg Cys His His His Ser Ser Ile Lys Ser Asn Ala Ser
 290 295 300
 Gly Arg Met Ser Thr Ser Thr Ser Met Arg Asn Cys Ser Pro Gln His
 305 310 315 320
 Ser Ser Pro Arg Ser Ala Ser Thr Ser Leu Gly Ser Thr His Glu Ser
 325 330 335
 Pro Glu Lys Ser Ser Ile Ser Arg Thr Asn Thr Trp Val Leu His His
 340 345 350
 Ala Thr Asn Asn Ser Asn Ser Gly Ala Cys Asn Gln Val Val Ile Ala
 355 360 365
 Asn Asn Thr Ser Gln Ser Ala Pro Asn Asn Gln Leu Asn Ser Ser Ala
 370 375 380
 Gln Pro Glu Val Thr Val Thr Lys Ser Ser Arg Arg Ser Ser Lys Ser
 385 390 395 400
 Tyr Lys Ser Phe Lys Lys Glu Arg Val Gln Ile Ser Val Gln Tyr Pro
 405 410 415
 Ser Ala Glu Arg Leu Asp Glu Leu Glu Gly Glu Leu Glu Gly Asp Ala
 420 425 430
 Thr Asn Asn Met Tyr Thr Val His Tyr Ser Val Ser Asn Gly Asn Ser
 435 440 445
 Leu Ser Asn His Ser Leu Met Pro Glu Gln Gln Ile Val Asp Ser Ser
 450 455 460
 Ser Gln Gln Gln Thr Ile Lys Gln Gln Gln Gln Leu Thr Val Asn Gln
 465 470 475 480

FC-11-PCT.ST25.txt

Gln Leu Asn Ser Gly Ser Ile Tyr Arg Pro Gln Asp Asn His His Leu
 485 490 495

Arg Val Thr Ser Gln Arg Leu Ala Pro Ser Pro Thr Leu Ser Lys Gly
 500 505 510

Met His Arg Arg Ser Ser Ser Cys Asp Ser Arg Asp Leu Ala Gly Phe
 515 520 525

Gln Leu Cys Glu Ser Ser Ser Pro Ser Pro Thr Arg Arg Ile Met Ser
 530 535 540

Gly Ser Leu Tyr Arg Asp Asp Ser Glu Leu Gly Ser Thr Ser Lys Leu
 545 550 555 560

Gln Gln Gln Asn Arg Lys Met Gly Lys Arg Asn Ile Lys Ala Gln Val
 565 570 575

Lys Arg Phe Arg Met Glu Thr Lys Ala Ala Lys Thr Leu Ala Ile Ile
 580 585 590

Val Gly Gly Phe Ile Val Cys Trp Phe Pro Phe Phe Thr Met Tyr Val
 595 600 605

Ile Arg Ala Phe Cys Pro Asp Cys Ile His Pro Val Leu Phe Ser Val
 610 615 620

Leu Phe Trp Leu Gly Tyr Cys Asn Ser Ala Ile Asn Pro Leu Ile Tyr
 625 630 635 640

Ala Leu Phe Ser Lys Asp Phe Arg Tyr Ala Phe Lys Arg Ile Ile Cys
 645 650 655

Arg Tyr Cys Phe Cys Cys Gly Asn Arg Thr Glu Ala Gln His Ser Gly
 660 665 670

Gly Ala Gly Gly Ser Arg Arg Gly Ser Asp Gly Ser Gln Met Lys Thr
 675 680 685

Asn Phe Arg Phe Asn Thr Ser Phe Asn Thr Lys Asn Cys Val Arg Gln
 690 695 700

Asp Ser Asp Asn Asp Val Thr Arg
 705 710

<210> 13
 <211> 2136
 <212> DNA

FC-11-PCT.ST25.txt

<213> Ctenocephalides felis

<400> 13

tcttgtgaca tcattatcac tatcttgacg aacgcagttt ttggtattaa aactgggtatt	60
aaacctaataa ttagttttca tttgagatcc atcggaccct cttctagaac caccagctcc	120
accgctgtgc tgggcctcgg tacgattacc gcaacaaaag cagtatctgc aaatgatgcg	180
cttgaaggcg tatctaaaat ctttgctaaa aagtgcataa atcagcggat tgatggcaga	240
attgcagtag ccgagccaga atagaaccga gaagagaaca ggatgaatgc agtctggaca	300
aaatgctctt attacgtaca ttgtgaaaaa gggaaaccag catacaataa aaccaccgac	360
aattattgca agtgtttttg cagctttcgt ctccattcga aaccgtttca cctgagcttt	420
tatattacgt ttgcccattt ttctattttg ctgctgcagt ttggaagtcg aacctaactc	480
gctatcatca cgataaagac ttccagacat tatccttctt gttggacttg gacttgaact	540
ttcgcataat tgaaaccag ccaaattctt actatcgcag ctgctggatc gcctatgcat	600
tcccttcgac agtgtaggag acggtgcaa tctttgcgac gtaactcgga gatgatgatt	660
atcctgtggc cgatagatgg aaccgaatt taattgctga ttcaccgtta attgttgttg	720
ttgcttaatg gtctgttgtt ggctcgaaga atcgactatt tgctgctctg gcatcaacga	780
atgatttgac aagctgttac cattggacac agagtagtgg acggtgtaca tgttgtttgt	840
agcatcacct tctaattcac ctccaattc atcaagtctt tctgcacttg gatactgcac	900
cgaaatttga actcttttct tcttaaagct cttatatgat ttcgaagatc ttcgactact	960
ttttgttaca gtgacttcag gctgggcact actatttaac tgattgtttg gtgcactttg	1020
acttgtatta ttggcgataa ctacttggtt acaagctcca gaattggaat tattggtcgc	1080
atgatgcaaa acccaggtgt tggctcctga tatagatgat ttttcaggtg attcgtgagt	1140
acttcctaag ctggtacttg cactacgtgg tgaactatgt tgtggagaac aattcctcat	1200
agaagtagat gtagacattc tccctgaagc attgctttta atggaagaat gatgatgaca	1260
tcttctattt tcagaaccac cccgtcctct atgaatcctt aaagttaggc gttgttcgtc	1320
aaatcgtcct ataccacgag aaccttttgt ggtcctgaat ccttggttga tagctctggt	1380
tgtcctgaca gctgctctat atatcctcca gtagaaaaat aacatgacaa acataggaat	1440
gtagaatgat cctagagcag aatacaccac atatcctgca tcattcgtca actcgcacgt	1500
ccacggacat gaagatatgt ctatcagatc ctccgattcc tttttatcct tccatccgac	1560
taaagggtgga aaacatatca caaaactaag aacccaaagc ccggctatga gtcccttagc	1620
ccttttcgta gacatgatgc tcggataagc aactggcctg gtgacagcga catatctatc	1680
caaggatatt gcgcacagat ttaatatcga agctgtgcac atccacacgt ccagggctaa	1740
ccaggctcgg caccagctgc ttccgaatat ccaaacttg aagacttccc aagttgcgct	1800
aaaaggcaaa accgcgatgc cgaccatcaa atcggcgact gcaagtgaca ctatgaacaa	1860

FC-11-PCT.ST25.txt

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gttggtcaca ctgcgcagtt tgctggagca gaacacggct gctatcacca gacaatttcc 1920
caggatcacc agcaaatacga tggtcagcaa aaccgtgaga cttgctaagg aagaaggact 1980
cagccagtcg acattttcaa tttgaggaca ttcagtccca tcatggttgt acaaagttgt 2040
cgaatttccc tgtcctgtgg taatggttgc cccagataag gaagtcccat aacttagcct 2100
gattgttgtc gtgttaatgt actccgaggc attcat 2136

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<210> 14
<211> 20
<212> DNA
<213> Artificial

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<220>
<223> Synthetic Primer

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<220>
<221> misc_feature
<222> (3)..(3)
<223> n = unknown

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<220>
<221> misc_feature
<222> (9)..(9)
<223> n = unknown

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<400> 14
gtngaygtnt ggatgtgyac 20

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<210> 15
<211> 18
<212> DNA
<213> Artificial

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<220>
<223> Synthetic Primer

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<220>
<221> misc_feature
<222> (4)..(4)
<223> n = unknown

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<220>
<221> misc_feature
<222> (16)..(16)
<223> n = unknown

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<400> 15
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<210> 16
<211> 22
<212> DNA
<213> Artificial

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<220>

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FC-11-PCT.ST25.txt

<223> Synthetic Primer

<400> 16

atgtgtggat gtgtacagct tc

22

<210> 17

<211> 22

<212> DNA

<213> Artificial

<220>

<223> Synthetic Primer

<400> 17

gtaatacgac tcactatagg gc

22

<210> 18

<211> 23

<212> DNA

<213> Artificial

<220>

<223> Synthetic Primer

<400> 18

aaatctgtgc gcaatatacct tgg

23

<210> 19

<211> 27

<212> DNA

<213> Artificial

<220>

<223> Synthetic Primer

<400> 19

ccatcctaatacgcactcact atagggc

27

<210> 20

<211> 22

<212> DNA

<213> Artificial

<220>

<223> Synthetic Primer

<400> 20

ggaagcagat cacaaaacta ag

22

<210> 21

<211> 22

<212> DNA

<213> Artificial

<220>

<223> Synthetic Primer

<400> 21

ccaaagcccg gctatgagtc cc

22

FC-11-PCT.ST25.txt

<210> 22
<211> 38
<212> DNA
<213> Artificial

<220>
<223> Synthetic Primer

<400> 22
aagaattcga tatgaatgcc tcggagtaca ttaacacg

38

<210> 23
<211> 37
<212> DNA
<213> Artificial

<220>
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<400> 23
ttctcgagcc tcttgatgaca tcattatcac tatcttg

37

<210> 24
<211> 36
<212> DNA
<213> Artificial

<220>
<223> Synthetic Primer

<400> 24
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36

<210> 25
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Synthetic Primer

<400> 25
cttggtaccg agctcggatc c

21

<210> 26
<211> 36
<212> DNA
<213> Artificial

<220>
<223> Synthetic Primer

<400> 26
ccttttctgg tcctgaatcc ttggttgata gctctg

36

<210> 27
<211> 21

FC-11-PCT.ST25.txt

<212> DNA
 <213> Artificial

<220>
 <223> Synthetic Primer

<400> 27
 agatgcatgc tcgagcggcc g 21

<210> 28
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<220>
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<400> 28
 atgaatgcct cggagtacat taacacgaca acaatcag 38

<210> 29
 <211> 37
 <212> DNA
 <213> Artificial

<220>
 <223> Synthetic Primer

<400> 29
 tcaccttggtg acatcattat cactatcttg acgaacg 37

<210> 30
 <211> 102
 <212> DNA
 <213> Rhipicephalus sanguineus

<220>
 <221> CDS
 <222> (1)..(102)

<400> 30
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 Ala Ile Ile Val Gly Ile Phe Ile Val Cys Trp Ile Thr Val His Thr
 1 5 10 15

ttt aga ttc ttt aag caa aca ctt ggc tac tgc aac tcg gcc ata aac 96
 Phe Arg Phe Phe Lys Gln Thr Leu Gly Tyr Cys Asn Ser Ala Ile Asn
 20 25 30

ccc aga 102
 Pro Arg

<210> 31
 <211> 34
 <212> PRT
 <213> Rhipicephalus sanguineus

<400> 31

FC-11-PCT.ST25.txt

Ala Ile Ile Val Gly Ile Phe Ile Val Cys Trp Ile Thr Val His Thr
 1 5 10 15

Phe Arg Phe Phe Lys Gln Thr Leu Gly Tyr Cys Asn Ser Ala Ile Asn
 20 25 30

Pro Arg

<210> 32
 <211> 102
 <212> DNA
 <213> Rhipicephalus sanguineus

<400> 32
 tctgggggttt atggccgagt tgcagtagcc aagtgtttgc ttaaagaatc taaaggatg 60
 cactgtaatc cagcacacga tgaagatgcc cacaatgatg gc 102

<210> 33
 <211> 499
 <212> DNA
 <213> Rhipicephalus sanguineus

<220>
 <221> CDS
 <222> (3)..(278)

<220>
 <221> misc_feature
 <222> (8)..(8)
 <223> n = unknown
 Xaa at location 2 = Tyr

<400> 33
 tg tct tan gag tca tca ccg tgg cat tcg ccc ttg gtg cgt gca ttc 47
 Ser Xaa Glu Ser Ser Pro Trp His Ser Pro Leu Val Arg Ala Phe
 1 5 10 15
 tgc gag cac tgc atc ccc aac ctg ctg ttc tcg gtc ttc ttc tgg ctc 95
 Cys Glu His Cys Ile Pro Asn Leu Leu Phe Ser Val Phe Phe Trp Leu
 20 25 30
 gga tac tgc aac tcg gcc atc aac ccg ctc atc tac gtg ctt gtc agc 143
 Gly Tyr Cys Asn Ser Ala Ile Asn Pro Leu Ile Tyr Val Leu Val Ser
 35 40 45
 aag gac ttt cgg ctg gcc ttc aag cgc atc ctg tgt cgc tgc cgc ctc 191
 Lys Asp Phe Arg Leu Ala Phe Lys Arg Ile Leu Cys Arg Cys Arg Leu
 50 55 60
 aaa gaa gga ggc gtc tcg tca ctc atc aaa cag atc cac atg ctc acc 239
 Lys Glu Gly Gly Val Ser Ser Leu Ile Lys Gln Ile His Met Leu Thr
 65 70 75
 gta ctt gac gac gca ccc ccg gac aac gcc gag tcg ccc tagaatcctg 288
 Val Leu Asp Asp Ala Pro Pro Asp Asn Ala Glu Ser Pro
 80 85 90

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gtcacagcct tctcctgccc ggcctatcgc ggcattctca tggggcgcca ctgcttcttt 348
gcacctcacc cgctcactgc accgcgtgtc tctgccgtag tgacattgtc ggtgtccatc 408
tcacggctgt aatgtctect tcttcaccca cgtgaatcac cactatagcc acagagcaaa 468
cgtgccagta ccaagagcgc ttctgccgca c 499

<210> 34
<211> 92
<212> PRT
<213> Rhipicephalus sanguineus

<220>
<221> misc_feature
<222> (2)..(2)
<223> The 'Xaa' at location 2 stands for Tyr.

<400> 34

Ser Xaa Glu Ser Ser Pro Trp His Ser Pro Leu Val Arg Ala Phe Cys
1 5 10 15

Glu His Cys Ile Pro Asn Leu Leu Phe Ser Val Phe Phe Trp Leu Gly
20 25 30

Tyr Cys Asn Ser Ala Ile Asn Pro Leu Ile Tyr Val Leu Val Ser Lys
35 40 45

Asp Phe Arg Leu Ala Phe Lys Arg Ile Leu Cys Arg Cys Arg Leu Lys
50 55 60

Glu Gly Gly Val Ser Ser Leu Ile Lys Gln Ile His Met Leu Thr Val
65 70 75 80

Leu Asp Asp Ala Pro Pro Asp Asn Ala Glu Ser Pro
85 90

<210> 35
<211> 499
<212> DNA
<213> Rhipicephalus sanguineus

<220>
<221> misc_feature
<222> (492)..(492)
<223> n = unknown

<400> 35
gtgcggcaga agcgcctcttg gtactggcac gtttgctctg tggctatagt ggtgattcac 60
gtgggtgagg aaggagacat tacagccgtg agatggacac cgacaatgtc actacggcag 120
agacacgcgg tgcagtgagc ggggtgaggtg caaagaagca gtggcgcccc atgagaatgc 180

FC-11-PCT.ST25.txt

cgcgatagcg cgggcaggag aaggctgtga ccaggattct agggcgactc ggcgttgctc 240
 ggggggtgctg cgtcaagtac ggtgagcatg tggatctgtt tgatgagtga cgagacgcct 300
 ccttctttga ggccggcagcg acacaggatg cgcttgaagg ccagccgaaa gtccttgctg 360
 acaagcacgt agatgagcgg gttgatggcc gagttgcagt atccgagcca gaagaagacc 420
 gagaacagca ggttggggat gcagtgctcg cagaatgcac gcaccaaggg cgaatgccac 480
 ggtgatgact cntaagaca 499

<210> 36
 <211> 286
 <212> DNA
 <213> Rhipicephalus sanguineus

<220>
 <221> CDS
 <222> (1)..(285)

<400> 36
 cgg ccc ggt agc aac atg aac gag acg tgc ctg tcc cgc gtg ccg cca 48
 Arg Pro Gly Ser Asn Met Asn Glu Thr Cys Leu Ser Arg Val Pro Pro
 1 5 10 15
 gag aag ctc cat gag ccg gtc act gtg gcc ctg ttc ttc gta ctg ggc 96
 Glu Lys Leu His Glu Pro Val Thr Val Ala Leu Phe Phe Val Leu Gly
 20 25 30
 tcc atc aat gga ctc gtc atc ttc ggt aac ctg ctg gtc att atc gcc 144
 Ser Ile Asn Gly Leu Val Ile Phe Gly Asn Leu Leu Val Ile Ile Ala
 35 40 45
 gtg ctg gcc tca aca aag ctg cgc acg gtc acc aac tac ttc gtg gtg 192
 Val Leu Ala Ser Thr Lys Leu Arg Thr Val Thr Asn Tyr Phe Val Val
 50 55 60
 tcc ttg gct gtg gcc gac ctc tcg gtt ggg ctc acc gtg ttg cca tac 240
 Ser Leu Ala Val Ala Asp Leu Ser Val Gly Leu Thr Val Leu Pro Tyr
 65 70 75 80
 tca att gtg ttg gag gtg ctc gag gtg tgg ctc ttc ggc caa cct g 286
 Ser Ile Val Leu Glu Val Leu Glu Val Trp Leu Phe Gly Gln Pro
 85 90 95

<210> 37
 <211> 95
 <212> PRT
 <213> Rhipicephalus sanguineus

<400> 37
 Arg Pro Gly Ser Asn Met Asn Glu Thr Cys Leu Ser Arg Val Pro Pro
 1 5 10 15
 Glu Lys Leu His Glu Pro Val Thr Val Ala Leu Phe Phe Val Leu Gly
 20 25 30

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Ser Ile Asn Gly Leu Val Ile Phe Gly Asn Leu Leu Val Ile Ile Ala
 35 40 45

Val Leu Ala Ser Thr Lys Leu Arg Thr Val Thr Asn Tyr Phe Val Val
 50 55 60

Ser Leu Ala Val Ala Asp Leu Ser Val Gly Leu Thr Val Leu Pro Tyr
 65 70 75 80

Ser Ile Val Leu Glu Val Leu Glu Val Trp Leu Phe Gly Gln Pro
 85 90 95

<210> 38
 <211> 286
 <212> DNA
 <213> Rhipicephalus sanguineus

<400> 38
 cagggttgccc gaagagccac acctcgagca cctccaacac aattgagtat ggcaacacgg 60
 tgagcccaac cgagaggtcg gccacagcca aggacaccac gaagtagttg gtgaccgtgc 120
 gcagctttgt tgaggccagc acggcgataa tgaccagcag gttaccgaag atgacgagtc 180
 cattgatgga gcccagtacg aagaacaggg ccacagtgac cggctcatgg agcttctctg 240
 gcggcacgcg ggacaggcac gtctcgttca tgttgctacc gggccg 286

<210> 39
 <211> 1443
 <212> DNA
 <213> Rhipicephalus sanguineus

<220>
 <221> CDS
 <222> (1)..(1440)

<400> 39
 atg aac gag acg tgc ctg tcc cgc gtg ccg cca gag aag ctc cat gag 48
 Met Asn Glu Thr Cys Leu Ser Arg Val Pro Pro Glu Lys Leu His Glu
 1 5 10 15
 ccg gtc act gtg gcc ctg ttc ttc gta ctg ggc tcc atc aat gga ctc 96
 Pro Val Thr Val Ala Leu Phe Phe Val Leu Gly Ser Ile Asn Gly Leu
 20 25 30
 gtc atc ttc ggt aac ctg ctg gtc att atc gcc gtg ctg gcc tca aca 144
 Val Ile Phe Gly Asn Leu Leu Val Ile Ile Ala Val Leu Ala Ser Thr
 35 40 45
 aag ctg cgc acg gtc acc aac tac ttc gtg gtg tcc ttg gct gtg gcc 192
 Lys Leu Arg Thr Val Thr Asn Tyr Phe Val Val Ser Leu Ala Val Ala
 50 55 60
 gac ctc tcg gtt ggg ctc acc gtg ttg cca tac tca att gtg ttg gag 240
 Asp Leu Ser Val Gly Leu Thr Val Leu Pro Tyr Ser Ile Val Leu Glu
 65 70 75 80

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gtg ctc gag gtg tgg atc ttc ggc cac acc tgg tgc cag ata tgg cta	288
Val Leu Glu Val Trp Ile Phe Gly His Thr Trp Cys Gln Ile Trp Leu	
85 90 95	
gct gtg gac gta tgg ctc tgc aca tca tcc atc ctg aat ctc tgc gcc	336
Ala Val Asp Val Trp Leu Cys Thr Ser Ser Ile Leu Asn Leu Cys Ala	
100 105 110	
atc agc gtg gac cgc tac ttg gcc atc acg cgg ccg gtt cgc tac cgg	384
Ile Ser Val Asp Arg Tyr Leu Ala Ile Thr Arg Pro Val Arg Tyr Arg	
115 120 125	
agc ctc atg tgc tgc cgc cgc gcc aag ttg ctc atc gtg gcg gtg tgg	432
Ser Leu Met Ser Ser Arg Arg Ala Lys Leu Leu Ile Val Ala Val Trp	
130 135 140	
gtg atc gcc ttt gtc atc tgc ttc ccg ccg ctc gtt gga tgg aac gac	480
Val Ile Ala Phe Val Ile Cys Phe Pro Pro Leu Val Gly Trp Asn Asp	
145 150 155 160	
ggc ggg tct caa aac agc gtg cct tac cac ggg tgc aac gag acc ttg	528
Gly Gly Ser Gln Asn Ser Val Pro Tyr His Gly Ser Asn Glu Thr Leu	
165 170 175	
cac aat tgc agc atc gct gcc gat ggc ccg ttg ccg ctc tgc aag tcc	576
His Asn Ser Ser Ile Ala Ala Asp Gly Pro Leu Pro Leu Cys Lys Ser	
180 185 190	
gca caa tgt gtg ctg ata aac aac aag ggc tac gtc atc tac tgc gct	624
Ala Gln Cys Val Leu Ile Asn Asn Lys Gly Tyr Val Ile Tyr Ser Ala	
195 200 205	
ctg ggc tct ttc tac ata ccg atg ctg ttc atg ctg ttt ttc aac tac	672
Leu Gly Ser Phe Tyr Ile Pro Met Leu Phe Met Phe Phe Asn Tyr	
210 215 220	
cgc ata tac cgc gca gcc atc cag act ggg cgc gcc ctt gaa cga ggt	720
Arg Ile Tyr Arg Ala Ala Ile Gln Thr Gly Arg Ala Leu Glu Arg Gly	
225 230 235 240	
ttc ata acc aca aag tca gga aag atc aag gga cgc aca acg gac cag	768
Phe Ile Thr Thr Lys Ser Gly Lys Ile Lys Gly Arg Thr Thr Asp Gln	
245 250 255	
agg ctc acg cta cgc gtc cac cgc ggt aac gat tcc gct atg aac gcc	816
Arg Leu Thr Leu Arg Val His Arg Gly Asn Asp Ser Ala Met Asn Ala	
260 265 270	
aag cga ggt agc gag cac ctc ggt gct gag acc tgc atc gat ggc atc	864
Lys Arg Gly Ser Glu His Leu Gly Ala Glu Thr Cys Ile Asp Gly Ile	
275 280 285	
gtc acc ggt cgt cgc cgg ccc gga ctc aag aag tgc cgc gac gag ccg	912
Val Thr Gly Arg Arg Arg Pro Gly Leu Lys Lys Ser Arg Asp Glu Pro	
290 295 300	
tca gcc agc gcc cgg tgc tca gcc agc aag acg cgt cag caa agt gac	960
Ser Ala Ser Ala Arg Ser Ser Ala Ser Lys Thr Arg Gln Gln Ser Asp	
305 310 315 320	
cag cgg acc acg cgc tgc gcg ccg ccc tgc ttc aag tgc aac agg ggc	1008
Gln Arg Thr Thr Arg Ser Ala Pro Pro Ser Phe Lys Ser Asn Arg Gly	
325 330 335	

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```

agc gcc cgc aac agt gga cgc aac ggc act tcc acg tct agc ggc ggc      1056
Ser Ala Arg Asn Ser Gly Arg Asn Gly Thr Ser Thr Ser Ser Gly Gly
                340                      345                      350

ggc aag ggc tcg cgt tcg agc aaa cgc agt caa cgg tgg cag gcc aag      1104
Gly Lys Gly Ser Arg Ser Ser Lys Arg Ser Gln Arg Trp Gln Ala Lys
                355                      360                      365

cga ttc cgc aca gag gcc aag gcc acc aag acc gtg ggc acc atc gtg      1152
Arg Phe Arg Thr Glu Ala Lys Ala Thr Lys Thr Val Gly Thr Ile Val
                370                      375                      380

ggg ggc ttt ata tgc tgc tgg ctg ccc ttc ttc aca gtg tac ctg gtg      1200
Gly Gly Phe Ile Cys Cys Trp Leu Pro Phe Phe Thr Val Tyr Leu Val
                385                      390                      395                      400

cgt gca ttc tgc gag cac tgc atc ccc aac ctg ctg ttc tcg gtc ttc      1248
Arg Ala Phe Cys Glu His Cys Ile Pro Asn Leu Leu Phe Ser Val Phe
                405                      410                      415

ttc tgg ctc gga tac tgc aac tcg gcc atc aac ccg ctc atc tac gtg      1296
Phe Trp Leu Gly Tyr Cys Asn Ser Ala Ile Asn Pro Leu Ile Tyr Val
                420                      425                      430

ctt gtc agc aag gac ttt cgg ctg gcc ttc aag cgc atc ctg tgt cgc      1344
Leu Val Ser Lys Asp Phe Arg Leu Ala Phe Lys Arg Ile Leu Cys Arg
                435                      440                      445

tgc cgc ctc aaa gaa gga ggc gtc tcg tca ctc atc aaa cag atc cac      1392
Cys Arg Leu Lys Glu Gly Gly Val Ser Ser Leu Ile Lys Gln Ile His
                450                      455                      460

atg ctc acc gta ctt gac gac gca ccc ccg gac aac gcc gag tcg ccc      1440
Met Leu Thr Val Leu Asp Asp Ala Pro Pro Asp Asn Ala Glu Ser Pro
                465                      470                      475                      480

tag                                                                 1443

```

```

<210> 40
<211> 480
<212> PRT
<213> Rhipicephalus sanguineus

```

```

<400> 40

```

```

Met Asn Glu Thr Cys Leu Ser Arg Val Pro Pro Glu Lys Leu His Glu
1          5          10          15

```

```

Pro Val Thr Val Ala Leu Phe Phe Val Leu Gly Ser Ile Asn Gly Leu
20          25          30

```

```

Val Ile Phe Gly Asn Leu Leu Val Ile Ile Ala Val Leu Ala Ser Thr
35          40          45

```

```

Lys Leu Arg Thr Val Thr Asn Tyr Phe Val Val Ser Leu Ala Val Ala
50          55          60

```

```

Asp Leu Ser Val Gly Leu Thr Val Leu Pro Tyr Ser Ile Val Leu Glu
65          70          75          80

```

FC-11-PCT.ST25.txt

Val Leu Glu Val Trp Ile Phe Gly His Thr Trp Cys Gln Ile Trp Leu
85 90 95

Ala Val Asp Val Trp Leu Cys Thr Ser Ser Ile Leu Asn Leu Cys Ala
100 105 110

Ile Ser Val Asp Arg Tyr Leu Ala Ile Thr Arg Pro Val Arg Tyr Arg
115 120 125

Ser Leu Met Ser Ser Arg Arg Ala Lys Leu Leu Ile Val Ala Val Trp
130 135 140

Val Ile Ala Phe Val Ile Cys Phe Pro Pro Leu Val Gly Trp Asn Asp
145 150 155 160

Gly Gly Ser Gln Asn Ser Val Pro Tyr His Gly Ser Asn Glu Thr Leu
165 170 175

His Asn Ser Ser Ile Ala Ala Asp Gly Pro Leu Pro Leu Cys Lys Ser
180 185 190

Ala Gln Cys Val Leu Ile Asn Asn Lys Gly Tyr Val Ile Tyr Ser Ala
195 200 205

Leu Gly Ser Phe Tyr Ile Pro Met Leu Phe Met Leu Phe Phe Asn Tyr
210 215 220

Arg Ile Tyr Arg Ala Ala Ile Gln Thr Gly Arg Ala Leu Glu Arg Gly
225 230 235 240

Phe Ile Thr Thr Lys Ser Gly Lys Ile Lys Gly Arg Thr Thr Asp Gln
245 250 255

Arg Leu Thr Leu Arg Val His Arg Gly Asn Asp Ser Ala Met Asn Ala
260 265 270

Lys Arg Gly Ser Glu His Leu Gly Ala Glu Thr Cys Ile Asp Gly Ile
275 280 285

Val Thr Gly Arg Arg Arg Pro Gly Leu Lys Lys Ser Arg Asp Glu Pro
290 295 300

Ser Ala Ser Ala Arg Ser Ser Ala Ser Lys Thr Arg Gln Gln Ser Asp
305 310 315 320

Gln Arg Thr Thr Arg Ser Ala Pro Pro Ser Phe Lys Ser Asn Arg Gly
325 330 335

FC-11-PCT.ST25.txt

Ser Ala Arg Asn Ser Gly Arg Asn Gly Thr Ser Thr Ser Ser Gly Gly
340 345 350

Gly Lys Gly Ser Arg Ser Ser Lys Arg Ser Gln Arg Trp Gln Ala Lys
355 360 365

Arg Phe Arg Thr Glu Ala Lys Ala Thr Lys Thr Val Gly Thr Ile Val
370 375 380

Gly Gly Phe Ile Cys Cys Trp Leu Pro Phe Phe Thr Val Tyr Leu Val
385 390 395 400

Arg Ala Phe Cys Glu His Cys Ile Pro Asn Leu Leu Phe Ser Val Phe
405 410 415

Phe Trp Leu Gly Tyr Cys Asn Ser Ala Ile Asn Pro Leu Ile Tyr Val
420 425 430

Leu Val Ser Lys Asp Phe Arg Leu Ala Phe Lys Arg Ile Leu Cys Arg
435 440 445

Cys Arg Leu Lys Glu Gly Gly Val Ser Ser Leu Ile Lys Gln Ile His
450 455 460

Met Leu Thr Val Leu Asp Asp Ala Pro Pro Asp Asn Ala Glu Ser Pro
465 470 475 480

<210> 41
<211> 1443
<212> DNA
<213> *Rhipicephalus sanguineus*

<400> 41
ctagggcgac tcggcggttgc ccgggggtgc gtcgtcaagt acggtgagca tgtggatctg 60
tttgatgagt gacgagacgc ctccttcttt gaggcggcag cgacacagga tgcgcttgaa 120
ggccagccga aagtccttgc tgacaagcac gtagatgagc gggttgatgg ccgagttgca 180
gtatccgagc cagaagaaga ccgagaacag caggttgggg atgcagtgtc cgcagaatgc 240
acgcaccagg tacactgtga agaagggcag ccagcagcat ataaagccac ccacgatggt 300
gcccacggtc ttggtggcct tggcctctgt gcggaatcgc ttggcctgcc accgttgact 360
gcgtttgctc gaacgcgagc ccttgccgcc gccgctagac gtggaagtgc cgttgcgtcc 420
actgttgccg gcgctgcccc tgttcgactt gaacgagggc ggccgagcgc gcgtgggtccg 480
ctggtcactt tgctgacgcg tcttgctggc tgacgaccgg gcgctggctg acggctcgtc 540
gcgcgacttc ttgagtcgag gccggcgagc accggtgagc atgccatcga tgcaggtctc 600

FC-11-PCT.ST25.txt

```

agcaccgagg tgctcgctac ctgcttggc gttcatagcg gaatcgttac cgcggtggac 660
gcgtagcgtg agcctctggt ccgttgtgcg tcccttgatc tttcctgact ttgtggttat 720
gaaacctcgt tcaagggcgc gccagtcctg gatggctgcg cggatatatgc ggtagttgaa 780
aaacagcatg aacagcatcg gtatgtagaa agagcccaga gccgagtaga tgacgtagcc 840
cttgttgttt atcagcacac attgtgcgga cttgcagagc ggcaacgggc catcggcagc 900
gatgctcgaa ttgtgcaagg tctcgttcga cccgtggtaa ggcacgctgt tttgagacct 960
gccgtcgttc catccaacga gcggcgggaa gcagatgaca aaggcgatca cccacaccgc 1020
cacgatgagc aacttggcgc ggcgcgacga catgaggctc cggtagcgaa ccggccgcgt 1080
gatggccaag tagcgggtcca cgctgatggc gcagagattc aggatggatg atgtgcagag 1140
ccatacgtcc acagctagcc atatctggca ccaggtgtgg ccgaagatcc acacctcgag 1200
cacctccaac acaattgagt atggcaacac ggtgagccca accgagaggt cggccacagc 1260
caaggacacc acgaagtagt tggtagaccg gcgcagcttt gttgaggcca gcacggcgat 1320
aatgaccagc aggttaccga agatgacgag tccattgatg gagcccagta cgaagaacag 1380
ggccacagtg accggctcat ggagcttctc tggcggcacg cgggacaggc acgtctcgtt 1440
cat 1443

```

```

<210> 42
<211> 33
<212> DNA
<213> Artificial

```

```

<220>
<223> Synthetic Primer

```

```

<400> 42
gccatcatyg tgggcrkstt catcktbgtc tgg 33

```

```

<210> 43
<211> 33
<212> DNA
<213> Artificial

```

```

<220>
<223> Synthetic Primer

```

```

<400> 43
gatcatsggr ttwayggcsg agttgcagta gcc 33

```

```

<210> 44
<211> 23
<212> DNA
<213> Artificial

```

```

<220>
<223> Synthetic Primer

```

```

<400> 44

```


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gctggctgcc attcttcacc gtg

23

<210> 45

<211> 27

<212> DNA

<213> Artificial

<220>

<223> Synthetic Primer

<400> 45

ccatcctaatac gactcact atagggc

27

<210> 46

<211> 24

<212> DNA

<213> Artificial

<220>

<223> Synthetic Primer

<400> 46

ggtgcgtgca ttctgcgagc actg

24

<210> 47

<211> 24

<212> DNA

<213> Artificial

<220>

<223> Synthetic Primer

<400> 47

agaagaccga gaacagcagg ttgg

24

<210> 48

<211> 29

<212> DNA

<213> Artificial

<220>

<223> Synthetic Primer

<400> 48

tggcaccagg tgtggccgaa gagccacac

29

<210> 49

<211> 24

<212> DNA

<213> Artificial

<220>

<223> Synthetic Primer

<400> 49

atgaacgaga cgtgcctgtc ccgc

24

<210> 50

FC-11-PCT.ST25.txt

<211> 24

<212> DNA

<213> Artificial

<220>

<223> Synthetic Primer

<400> 50

ctagggcgac gcggcggtgt ccgg

24